

## SEQUENCE LISTING

<110> Syngenta Participations AG  
 Shen, Zhicheng  
 Warren, Gregory  
 Shotkoski, Frank  
 Kramer, Vance

<120> Novel Vip3 Toxins and Methods of Use

<130> 60163PCT

<150> US 60/362250  
 <151> 2002-03-06

<160> 33

<170> PatentIn version 3.2

<210> 1  
 <211> 2367  
 <212> DNA  
 <213> Bacillus thuringiensis

<220>  
 <221> misc\_feature  
 <222> (1)..(2367)  
 <223> Native vip3C coding sequence.

An "r" at position 2213 represents the nucleotide g or a.

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tacttaagta agcaattgca agaaatttct gataaattag atattattaa cgtaaattgt      480
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tcatttgaaa acgtttctat taaataa 2367

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&lt;210&gt; 2

&lt;211&gt; 788

&lt;212&gt; PRT

<213> *Bacillus thuringiensis*

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (1)..(788)

&lt;223&gt; Vip3C Toxin

The Xaa at position 738 is either the amino acid Glu or Gly.

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Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg Ala Leu Pro Ser Phe

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                     20                      25                      30  
 Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asn Leu Thr Leu  
                     35                      40                      45  
 Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Glu Ile Ser Gly Lys  
                     50                      55                      60  
 Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn  
                     65                      70                      75                      80  
 Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln  
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 Met Leu His Ile Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val  
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 Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys  
                     130                      135                      140  
 Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val  
                     145                      150                      155                      160  
 Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile  
                     165                      170                      175  
 Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr  
                     180                      185                      190  
 Thr Leu Lys Val Lys Lys Asp Ser Ser Pro Ala Asp Ile Leu Asp Glu  
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 Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val  
                     210                      215                      220  
 Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly  
                     225                      230                      235                      240  
 Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile  
                     245                      250                      255  
 Ala Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr  
                     260                      265                      270

Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr  
 275 280 285

Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Gly Ile Asp Tyr Thr  
 290 295 300

Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val  
 305 310 315 320

Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala  
 325 330 335

Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys  
 340 345 350

Pro Gly His Ala Leu Val Gly Phe Glu Met Ser Asn Asp Ser Ile Thr  
 355 360 365

Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp  
 370 375 380

Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Thr Asp Lys Leu Phe  
 385 390 395 400

Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe  
 405 410 415

Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys  
 420 425 430

Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly  
 435 440 445

Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr  
 450 455 460

Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val  
 465 470 475 480

Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala  
 485 490 495

Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg  
 500 505 510

Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile  
 515 520 525

Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile  
 530 535 540

Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr  
 545 550 555 560

Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His  
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Lys Asp Gly Gly Phe Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys  
 580 585 590

Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His  
 595 600 605

Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn  
 610 615 620

Asn Leu Lys Asp Tyr Gln Thr Ile Thr Lys Arg Phe Thr Thr Gly Thr  
 625 630 635 640

Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu  
 645 650 655

Ala Trp Gly Asp Lys Phe Thr Ile Leu Glu Ile Lys Pro Ala Glu Asp  
 660 665 670

Leu Leu Ser Pro Glu Leu Ile Asn Pro Asn Ser Trp Ile Thr Thr Pro  
 675 680 685

Gly Ala Ser Ile Ser Gly Asn Lys Leu Phe Ile Asn Leu Gly Thr Asn  
 690 695 700

Gly Thr Phe Arg Gln Ser Leu Ser Leu Asn Ser Tyr Ser Thr Tyr Ser  
 705 710 715 720

Ile Ser Phe Thr Ala Ser Gly Pro Phe Asn Val Thr Val Arg Asn Ser  
 725 730 735

Arg Xaa Val Leu Phe Glu Arg Ser Asn Leu Met Ser Ser Thr Ser His  
 740 745 750

Ile Ser Gly Thr Phe Lys Thr Glu Ser Asn Asn Thr Gly Leu Tyr Val  
 755 760 765

Glu Leu Ser Arg Arg Ser Gly Gly Gly Gly His Ile Ser Phe Glu Asn  
 770 775 780

Val Ser Ile Lys  
785

<210> 3  
<211> 2367  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Maize optimized vip3C coding sequence.

An "r" at positions 2213 and 2214 represents the nucleotide g or a.

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gacaccggcg gcaacctcac cctcgacgag atcctcaaga accagcagct cctcaacgag      180
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 ttcgagcgct ccaacctcat gtctccacc tcccacatct ccggcacctt caagaccgag 2280  
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<210> 4  
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 <212> DNA  
 <213> *Bacillus thuringiensis*

<220>  
 <221> misc\_feature  
 <222> (1)..(2370)  
 <223> vip3A(a) native coding sequence.

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<210> 5
<211> 789
<212> PRT
<213> Bacillus thuringiensis

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&lt;220&gt;

&lt;221&gt; MISC FEATURE

&lt;222&gt; (1)..(789)

&lt;223&gt; Vip3A toxin

&lt;400&gt; 5

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 20 25 30

Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu  
 35 40 45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys  
 50 55 60

Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn  
 65 70 75 80

Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln  
 85 90 95

Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr  
 100 105 110

Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val  
 115 120 125

Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys  
 130 135 140

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val  
 145 150 155 160

Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile  
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Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr  
 180 185 190

Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu  
 195 200 205

Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val  
 210 215 220

Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly  
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225                      230                      235                      240  
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 Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr  
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 Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr  
                                  275                                   280                                   285  
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                                  290                                   295                                   300  
 Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val  
                                  305                                   310                                   315                                   320  
 Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala  
                                  325                                   330                                   335  
 Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys  
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                                  370                                   375                                   380  
 Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu  
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 Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe  
                                  405                                   410                                   415  
 Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys  
                                  420                                   425                                   430  
 Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly  
                                  435                                   440                                   445  
 Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr  
                                  450                                   455                                   460  
 Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val  
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 Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala  
                                  485                                   490                                   495

Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg  
 500 505 510

Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile  
 515 520 525

Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile  
 530 535 540

Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr  
 545 550 555 560

Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His  
 565 570 575

Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys  
 580 585 590

Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His  
 595 600 605

Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn  
 610 615 620

Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr  
 625 630 635 640

Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu  
 645 650 655

Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys  
 660 665 670

Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly  
 675 680 685

Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg  
 690 695 700

Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg  
 705 710 715 720

Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser  
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Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val  
 740 745 750

Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr Ile Glu  
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Asp Val Ser Ile Lys  
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<210> 6  
 <211> 2364  
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 <213> *Bacillus thuringiensis*

<220>  
 <221> misc\_feature  
 <222> (1)..(2364)  
 <223> vip3B native coding sequence.

<400> 6  
 atgaacaaga ataatactaa attaaacgca agggccttac cgagttttat tgattatattt 60  
 aatggcattt atggatttgc cactggtatc aaagacatta tgaacatgat ttttaaaacg 120  
 gatacaggtg gaaatctaac cctagacgaa attttaaaaa atcagcagtt attaaatgag 180  
 atttctggta aattggatgg ggtaaatggg agcttaaacg atcttatcgc acagggaaac 240  
 ttaaatacag aattatctaa ggaaatctta aaaattgcaa atgagcagaa tcaagtctta 300  
 aatgatgtta ataacaaact taatgcgata aatacaatgc ttcacatata tctacctaaa 360  
 attacatcta tggtaaatga tgtaatgaaa caaaattatg cactaagtct gcaaatagaa 420  
 tacctaagta aacaattgca agaaatttcc gacaagttag atgtcattaa cgtgaatgta 480  
 cttattaact ctacacttac tgaaattaca cctgcgtatc aacggatgaa atatgtaaat 540  
 gaaaaatttg aagatttaac ttttgctaca gaaaccactt taaaagtaaa aaagaatagc 600  
 tcccctgcag atattcttga tgagttaact gagttaactg aactagcgaa aagtgttaaca 660  
 aaaaatgacg tggatggttt tgaattttac cttatacat tccacgatgt aatggtagga 720  
 aacaatttat tcgggcgttc agcttttaaaa actgcttcgg aattaatcgc taaagaaaat 780  
 gtgaaaacaa gtggcagtga ggtaggaaat gtttataatt tcttaattgt attaacagct 840  
 ctgcaagcaa aagcttttct tactttaaca acatgccgga aattattagg cttagcagat 900  
 attgattata ctttcattat gaatgaacat ttagataagg aaaaagagga atttagagta 960  
 aatatccttc ctacactttc taatactttt tctaataccta actatgcaaa agctaaagga 1020  
 agcaatgaag atgcaaagat aattgtggaa gctaaaccag gatatgcttt gggttgattt 1080  
 gaaatgagca atgattcaat cacagtatta aaagcatatc aggctaagct aaaacaagat 1140  
 tatcaagttg ataaagattc gttatcagaa attgtctatg gtgatatgga taaattattg 1200

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tgccccggatc aatctgaaca aatatattat acaaataaca ttgcttttcc caatgaatat 1260
gtaattacta aaattacttt tactaaaaaa atgaatagtt taagatatga ggcaacagct 1320
aatttttatg attcttctac aggggatatt gatctaaata agacaaaagt agaatcaagt 1380
gaagcagagt atagtacgct aagtgctagt actgatggag tctatatgcc gttaggtatt 1440
atcagtgaac catttttgac tccaattaat gggtttgga tctagtcga tgaaaattca 1500
aaattagtaa atttaacatg taaatcatat ttaagagagg tattattagc aacagactta 1560
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aatgggaact tagagggaga aaacttagag ccgtggaaag caaataacaa aaatgcgtat 1680
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gtaaagggaa aagcttctat tcttttgaaa gatgaaaaaa atggtgattg catttatgaa 1860
gatacaata atgggtttaga agattttcaa accattacta aaagttttat tacaggaacg 1920
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aactttacta tttcagaaat taggctttcc gaagatttat taagtccaga attgataaat 2040
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agtaatgtga atggaacttt tcgacaaaac ctttcgtttag aaagctattc aacttatagt 2160
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tttgaaaaaa attatccgca gctttcacct aaagatattt ctgaaaaatt cacaactgca 2280
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ttccggaatt tttcgattaa gtga 2364

```

```

<210> 7
<211> 787
<212> PRT
<213> Bacillus thuringiensis

```

```

<220>
<221> MISC_FEATURE
<222> (1)..(787)
<223> Vip3B Toxin

```

```

<400> 7

```

```

Met Asn Lys Asn Asn Thr Lys Leu Asn Ala Arg Ala Leu Pro Ser Phe
1          5          10          15

```

```

Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp
20          25          30

```

```

Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asn Leu Thr Leu
35          40          45

```

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Glu Ile Ser Gly Lys  
50 55 60

Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn  
65 70 75 80

Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln  
85 90 95

Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asn Ala Ile Asn Thr  
100 105 110

Met Leu His Ile Tyr Leu Pro Lys Ile Thr Ser Met Leu Asn Asp Val  
115 120 125

Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys  
130 135 140

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Val Ile Asn Val Asn Val  
145 150 155 160

Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Met  
165 170 175

Lys Tyr Val Asn Glu Lys Phe Glu Asp Leu Thr Phe Ala Thr Glu Thr  
180 185 190

Thr Leu Lys Val Lys Lys Asn Ser Ser Pro Ala Asp Ile Leu Asp Glu  
195 200 205

Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val  
210 215 220

Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly  
225 230 235 240

Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile  
245 250 255

Ala Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr  
260 265 270

Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr  
275 280 285

Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr  
290 295 300

Phe Ile Met Asn Glu His Leu Asp Lys Glu Lys Glu Glu Phe Arg Val  
305 310 315 320

Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala  
325 330 335

Lys Ala Lys Gly Ser Asn Glu Asp Ala Lys Ile Ile Val Glu Ala Lys  
340 345 350

Pro Gly Tyr Ala Leu Val Gly Phe Glu Met Ser Asn Asp Ser Ile Thr  
355 360 365

Val Leu Lys Ala Tyr Gln Ala Lys Leu Lys Gln Asp Tyr Gln Val Asp  
370 375 380

Lys Asp Ser Leu Ser Glu Ile Val Tyr Gly Asp Met Asp Lys Leu Leu  
385 390 395 400

Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Ala Phe  
405 410 415

Pro Asn Glu Tyr Val Ile Thr Lys Ile Thr Phe Thr Lys Lys Met Asn  
420 425 430

Ser Leu Arg Tyr Glu Ala Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly  
435 440 445

Asp Ile Asp Leu Asn Lys Thr Lys Val Glu Ser Ser Glu Ala Glu Tyr  
450 455 460

Ser Thr Leu Ser Ala Ser Thr Asp Gly Val Tyr Met Pro Leu Gly Ile  
465 470 475 480

Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Ile Val Val  
485 490 495

Asp Glu Asn Ser Lys Leu Val Asn Leu Thr Cys Lys Ser Tyr Leu Arg  
500 505 510

Glu Val Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile  
515 520 525

Val Pro Pro Ile Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Asn Leu  
530 535 540

Glu Gly Glu Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr  
545 550 555 560

Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His  
15

565

570

575

Lys Asp Gly Glu Phe Ser Gln Phe Ile Gly Asp Lys Leu Lys Ser Lys  
 580 585 590

Thr Glu Tyr Val Ile Gln Tyr Ile Val Lys Gly Lys Ala Ser Ile Leu  
 595 600 605

Leu Lys Asp Glu Lys Asn Gly Asp Cys Ile Tyr Glu Asp Thr Asn Asn  
 610 615 620

Gly Leu Glu Asp Phe Gln Thr Ile Thr Lys Ser Phe Ile Thr Gly Thr  
 625 630 635 640

Asp Ser Ser Gly Val His Leu Ile Phe Asn Ser Gln Asn Gly Asp Glu  
 645 650 655

Ala Phe Gly Glu Asn Phe Thr Ile Ser Glu Ile Arg Leu Ser Glu Asp  
 660 665 670

Leu Leu Ser Pro Glu Leu Ile Asn Ser Asp Ala Trp Val Gly Ser Gln  
 675 680 685

Gly Thr Trp Ile Ser Gly Asn Ser Leu Thr Ile Asn Ser Asn Val Asn  
 690 695 700

Gly Thr Phe Arg Gln Asn Leu Ser Leu Glu Ser Tyr Ser Thr Tyr Ser  
 705 710 715 720

Met Asn Phe Asn Val Asn Gly Phe Ala Lys Val Thr Val Arg Asn Ser  
 725 730 735

Arg Glu Val Leu Phe Glu Lys Asn Tyr Pro Gln Leu Ser Pro Lys Asp  
 740 745 750

Ile Ser Glu Lys Phe Thr Thr Ala Ala Asn Asn Thr Gly Leu Tyr Val  
 755 760 765

Glu Leu Ser Arg Phe Thr Ser Gly Gly Ala Ile Asn Phe Arg Asn Phe  
 770 775 780

Ser Ile Lys  
 785

<210> 8  
 <211> 2407  
 <212> DNA  
 <213> Bacillus thuringiensis



<220>  
 <221> misc.feature  
 <222> (1)..(2406)  
 <223> vip3Z native coding sequence.

<400> 8  
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 ggtgggtggtta atttaacact agatgaaatt ttaaagaatc aagatttatt aaatcaaadc 180  
 tcagataaac tcgatggaat taatggagat ttaggtgatc ttattgcaca aggcaattta 240  
 aattcagaac taactaagga attattaaaa attgcgaatg agcagaatct gatgttaaatt 300  
 aatgttaatg ctcaacttaa ttcaataaat tcaacactta acacctatct gccaaaaatt 360  
 acatctatgc taagtgaggt aatgaaacaa aactatgtat taagtctaca aatagaattt 420  
 cttagtgaac aattacaaga aatatcagat aaacttgatg ttatcaattt aaatgtatta 480  
 attaactcta cattgacaga aattacgcct gcatatcaac gtattaaata tgtaaattgat 540  
 aaatttgatg aattgacttc tactgtggaa aaaaatccga aaattaatca agataatttt 600  
 actgaagatg ttattgataa ttttaactgat ttaactgaac tagcacgaag tgtaacgaga 660  
 aatgatatgg atagttttga attttatatt aaaactttcc atgatgtgat gataggaaat 720  
 aattttattca gtcgttctgc attaaaaact gcttcagaat taattgctaa ggaaaatata 780  
 cactactatgg gaagtgaat tggtaatgtc tacactttta tggttgtttt gacttcctta 840  
 caagcaaaag cgttcctaac ttttaactgca tgccgtaaatt tattaggatt aacagatatc 900  
 gattatacac aaattatgaa tgaaaattta aatagagaaa aagagggaatt tcgcttaaat 960  
 attcttccta cacttttctaa tgatttttct aatcctaatt atacagaaac ttttaggaagt 1020  
 gatctttag atcctattgt tacgttagaa gctgatcctg gttatgcttt aatagggttt 1080  
 gagattctca atgatccact tccagtatta aaagtatatc aggcaaagct aaaaccaaatt 1140  
 tatcaagtcg acaaagagtc gattatggaa aatatttatg gaaatatcca caaactactt 1200  
 tgtccaaaac aacgtcacca aaaatattat ataaaagaca ttacatttcc tgaagggttat 1260  
 gtaatcacca aaattgtttt tgaaaaaaa ttgaatctat taggatatga agtaacagca 1320  
 aatctttatg acccatttac aggaagtatc gatttgaata agactattct agaatcatgg 1380  
 aaggaagaat gctgtgaaga agaattgctgt gaagaagaat gctgtgaaga agaattgctgt 1440  
 gaagaattat ataaaattat agaggcggat actaacggtg tttatatgcc gttggggagta 1500  
 attagtgaac cttttttaac accaatctat agtttttaac taattattga cgaaagaaca 1560  
 aagagaatat ctttagcggg taaatcttat ttacgtgaat ctttactagc cacagattta 1620  
 gtttaataaag atacgaattt aattccttca cccaatggtt tcattaacag tattgtggaa 1680  
 aattggaata taacatcgga taatatagag ccctggaaag cgaataataa aaatgcatat 1740  
 gtcgataaga cggatgacat ggtgggattt aactctttat atactcataa ggatggggaa 1800

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ttcttgcaat ttattggagc taagttaaag gctaaaactg agtatatcat tcaatatact 1860
gtaaaagggg gtccggaagt ttatttgaaa aacaataaag gtatctttta tgaggataca 1920
acaaataaat ttgatacggt tcaaactata actaaaaagt tcaattcagg agtagatcca 1980
tccgaaatat atctagtttt taaaaatcaa attggatatg aagcatgggg aaataaat 2040
attatactag aaatcaagtc atttgaaacc ctaccacaaa tattaaaacc tgaaaattgg 2100
atgccttttg gtaatgctga gattaaagaa gatggaaaaa ttgagatttc aggtaatgga 2160
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aaaggaaaag ggagagtagc gatacaaact caaagctccc atataaatgt accagctaca 2280
aacgaagagg tttctacaat gattacaact agaaacttat acggtgaagg tatgatatac 2340
ctatttaatg atgacgtgga gaactccaaa gttatttttt cggatgtatc tctagttaaa 2400
gaatagg 2407

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```

<210> 9
<211> 801
<212> PRT
<213> Bacillus thuringiensis

```

```

<220>
<221> MISC_FEATURE
<222> (1)..(801)
<223> Vip3Z toxin

```

```

<400> 9

```

```

Met Asn Asn Thr Lys Leu Asn Ala Arg Ala Leu Pro Ser Phe Ile Asp
1           5           10           15

```

```

Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp Ile Met
          20           25           30

```

```

Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Gly Asn Leu Thr Leu Asp
          35           40           45

```

```

Glu Ile Leu Lys Asn Gln Asp Leu Leu Asn Gln Ile Ser Asp Lys Leu
50           55           60

```

```

Asp Gly Ile Asn Gly Asp Leu Gly Asp Leu Ile Ala Gln Gly Asn Leu
65           70           75           80

```

```

Asn Ser Glu Leu Thr Lys Glu Leu Leu Lys Ile Ala Asn Glu Gln Asn
          85           90           95

```

```

Leu Met Leu Asn Asn Val Asn Ala Gln Leu Asn Ser Ile Asn Ser Thr
          100          105          110

```

Leu Asn Thr Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Glu Val Met  
 115 120 125

Lys Gln Asn Tyr Val Leu Ser Leu Gln Ile Glu Phe Leu Ser Glu Gln  
 130 135 140

Leu Gln Glu Ile Ser Asp Lys Leu Asp Val Ile Asn Leu Asn Val Leu  
 145 150 155 160

Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile Lys  
 165 170 175

Tyr Val Asn Asp Lys Phe Asp Glu Leu Thr Ser Thr Val Glu Lys Asn  
 180 185 190

Pro Lys Ile Asn Gln Asp Asn Phe Thr Glu Asp Val Ile Asp Asn Leu  
 195 200 205

Thr Asp Leu Thr Glu Leu Ala Arg Ser Val Thr Arg Asn Asp Met Asp  
 210 215 220

Ser Phe Glu Phe Tyr Ile Lys Thr Phe His Asp Val Met Ile Gly Asn  
 225 230 235 240

Asn Leu Phe Ser Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile Ala  
 245 250 255

Lys Glu Asn Ile His Thr Met Gly Ser Glu Ile Gly Asn Val Tyr Thr  
 260 265 270

Phe Met Val Val Leu Thr Ser Leu Gln Ala Lys Ala Phe Leu Thr Leu  
 275 280 285

Thr Ala Cys Arg Lys Leu Leu Gly Leu Thr Asp Ile Asp Tyr Thr Gln  
 290 295 300

Ile Met Asn Glu Asn Leu Asn Arg Glu Lys Glu Glu Phe Arg Leu Asn  
 305 310 315 320

Ile Leu Pro Thr Leu Ser Asn Asp Phe Ser Asn Pro Asn Tyr Thr Glu  
 325 330 335

Thr Leu Gly Ser Asp Leu Val Asp Pro Ile Val Thr Leu Glu Ala Asp  
 340 345 350

Pro Gly Tyr Ala Leu Ile Gly Phe Glu Ile Leu Asn Asp Pro Leu Pro  
 355 360 365

Val Leu Lys Val Tyr Gln Ala Lys Leu Lys Pro Asn Tyr Gln Val Asp  
 19

370

375

380

Lys Glu Ser Ile Met Glu Asn Ile Tyr Gly Asn Ile His Lys Leu Leu  
 385 390 395 400

Cys Pro Lys Gln Arg His Gln Lys Tyr Tyr Ile Lys Asp Ile Thr Phe  
 405 410 415

Pro Glu Gly Tyr Val Ile Thr Lys Ile Val Phe Glu Lys Lys Leu Asn  
 420 425 430

Leu Leu Gly Tyr Glu Val Thr Ala Asn Leu Tyr Asp Pro Phe Thr Gly  
 435 440 445

Ser Ile Asp Leu Asn Lys Thr Ile Leu Glu Ser Trp Lys Glu Glu Cys  
 450 455 460

Cys Glu Glu Glu Cys Cys Glu Glu Glu Cys Cys Glu Glu Glu Cys Cys  
 465 470 475 480

Glu Glu Leu Tyr Lys Ile Ile Glu Ala Asp Thr Asn Gly Val Tyr Met  
 485 490 495

Pro Leu Gly Val Ile Ser Glu Thr Phe Leu Thr Pro Ile Tyr Ser Phe  
 500 505 510

Lys Leu Ile Ile Asp Glu Arg Thr Lys Arg Ile Ser Leu Ala Gly Lys  
 515 520 525

Ser Tyr Leu Arg Glu Ser Leu Leu Ala Thr Asp Leu Val Asn Lys Asp  
 530 535 540

Thr Asn Leu Ile Pro Ser Pro Asn Gly Phe Ile Asn Ser Ile Val Glu  
 545 550 555 560

Asn Trp Asn Ile Thr Ser Asp Asn Ile Glu Pro Trp Lys Ala Asn Asn  
 565 570 575

Lys Asn Ala Tyr Val Asp Lys Thr Asp Asp Met Val Gly Phe Asn Ser  
 580 585 590

Leu Tyr Thr His Lys Asp Gly Glu Phe Leu Gln Phe Ile Gly Ala Lys  
 595 600 605

Leu Lys Ala Lys Thr Glu Tyr Ile Ile Gln Tyr Thr Val Lys Gly Ser  
 610 615 620

Pro Glu Val Tyr Leu Lys Asn Asn Lys Gly Ile Phe Tyr Glu Asp Thr  
 625 630 635 640

Thr Asn Lys Phe Asp Thr Phe Gln Thr Ile Thr Lys Lys Phe Asn Ser  
645 650 655

Gly Val Asp Pro Ser Glu Ile Tyr Leu Val Phe Lys Asn Gln Ile Gly  
660 665 670

Tyr Glu Ala Trp Gly Asn Lys Phe Ile Ile Leu Glu Ile Lys Ser Phe  
675 680 685

Glu Thr Leu Pro Gln Ile Leu Lys Pro Glu Asn Trp Met Pro Phe Gly  
690 695 700

Asn Ala Glu Ile Lys Glu Asp Gly Lys Ile Glu Ile Ser Gly Asn Gly  
705 710 715 720

Thr Met Thr Gln Asn Ile Gln Leu Glu Gln Asn Ser Lys Tyr His Leu  
725 730 735

Arg Phe Ser Val Lys Gly Lys Gly Arg Val Ala Ile Gln Thr Gln Ser  
740 745 750

Ser His Ile Asn Val Pro Ala Thr Asn Glu Glu Val Ser Thr Met Ile  
755 760 765

Thr Thr Arg Asn Leu Tyr Gly Glu Gly Met Ile Tyr Leu Phe Asn Asp  
770 775 780

Asp Val Glu Asn Ser Lys Val Ile Phe Ser Asp Val Ser Leu Val Lys  
785 790 795 800

Glu

<210> 10

<211> 2367

<212> DNA

<213> Artificial Sequence

<220>

<223> vip3A-C Hybrid toxin coding sequence.

<400> 10

atgaacaaga ataatactaa attaagcaca agagccttac caagttttat tgattatttt 60

aatggcattt atggatttgc cactggtatc aaagacatta tgaacatgat ttttaaaacg 120

gatacaggtg gtgatctaac cctagacgaa attttaaaga atcagcagtt actaaatgat 180

atttctggta aattggatgg ggtgaatgga agcttaaagt atcttatcgc acagggaaac 240

ttaaatacag aattatctaa ggaaatatta aaaattgcaa atgaacaaaa tcaagtttta 300

aatgatgtta ataacaaact cgatgcgata aatacgatgc ttcgggtata tctacctaaa	360
attacctcta tgttgagtga tgtaatgaaa caaaattatg cgctaagtct gcaaatagaa	420
tacttaagta aacaattgca agagatttct gataagttgg atattattaa tgtaaagtga	480
cttattaact ctacacttac tgaaattaca cctgcgtatc aaaggattaa atatgtgaac	540
gaaaaatttg aggaattaac ttttgctaca gaaactagtt caaaagtaaa aaaggatggc	600
tctcctgcag atattcttga tgagttaact gagttaactg aactagcgaa aagtgtaca	660
aaaaatgatg tggatggttt tgaattttac cttaatatcat tccacgatgt aatggtagga	720
aataatttat tccggcgctc agcttttaaaa actgcatcgg aattaattac taaagaaaat	780
gtgaaaacaa gtggcagtga ggtcggaaat gtttataact tcttaattgt attaacagct	840
ctgcaagcaa aagcttttct tactttaaca acatgccgaa aattattagg cttagcagat	900
attgattata cttctattat gaatgaacat ttaaataagg aaaaagagga atttagagta	960
aacatcctcc ctacactttc taatactttt tctaataccta attatgcaaa agttaagga	1020
agtgatgaag atgcaaagat gattgtggaa gctaaaccag gacatgcatt gattgggttt	1080
gaaattagta atgattcaat tacagtatta aaagtatatg aggctaagct aaaacaaaat	1140
tatcaagtcg ataaggattc cttatcggaa gttatttatg gtgatatgga taaattattg	1200
tgcccagatc aatctgaaca aatctattat acaaataaca tagtatttcc aaatgaatat	1260
gtaattacta aaattgattt cactaaaaaa atgaaaactt taagatatga ggtaacagcg	1320
aatttttatg attcttctac aggagaaatt gacttaaata agaaaaaagt agaatcaagt	1380
gaagcggagt atagaacggt aagtgcta at gatgatgggg tgtatatgcc gttaggtgtc	1440
atcagtgaaa catTTTTgac tccgattaat gggtttgcc tccaagctga tgaaaattca	1500
agattaatta ctttaacatg taaatcatat ttaagagaac tactgctagc aacagactta	1560
agcaataaag aaactaaatt gatcgtcccg ccaagtgggt ttattagcaa tattgtagag	1620
aacgggtcca tagaagagga caatttagag ccgtggaaag caaataataa gaatgcgtat	1680
gtagatcata caggcggagt gaatggaact aaagctttat atgttcataa ggacggagga	1740
atttcacaat ttattggaga taagttaaaa ccgaaaactg agtatgtaat ccaatatact	1800
gttaaaggaa aaccttctat tcattttaaaa gatgaaaata ctggatatat tcattatgaa	1860
gatacaaata ataatttaga agattatcaa actattaata aacgttttac tacaggaact	1920
gatttaaagg gagtgtattt aattttaaaa agtcaaaatg gagatgaagc ttggggagat	1980
aaatttacaa ttttagaaat taagcctgcg gaggatttat taagcccaga attaattaat	2040
ccgaattctt ggattacgac tccaggggct agcatttcag gaaataaact tttcattaac	2100
ttggggacaa atgggacctt tagacaaagt ctttcattaa acagttattc aacttatagt	2160
ataagcttta ctgcatcagg accatttaat gtgacggtaa gaaattctag gggagtatta	2220
tttgaacgaa gcaaccttat gtcttcaact agtcatattt ctgggacatt caaaactgaa	2280

tcgaataata ccgattata tgtagaactt tcccgtcgct ctggtggtgg tggatcatata 2340  
 tcatttgaaa acgtttctat taaataa 2367

<210> 11  
 <211> 788  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Hybrid Vip3A-C toxin

<400> 11

Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg Ala Leu Pro Ser Phe  
 1 5 10 15

Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp  
 20 25 30

Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu  
 35 40 45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys  
 50 55 60

Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn  
 65 70 75 80

Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln  
 85 90 95

Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr  
 100 105 110

Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val  
 115 120 125

Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys  
 130 135 140

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val  
 145 150 155 160

Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile  
 165 170 175

Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr  
 180 185 190

Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu  
 23

195

200

205

Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val  
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Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly  
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Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln  
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Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr  
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Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu  
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Ala Trp Gly Asp Lys Phe Thr Ile Leu Glu Ile Lys Pro Ala Glu Asp  
660 665 670

Leu Leu Ser Pro Glu Leu Ile Asn Pro Asn Ser Trp Ile Thr Thr Pro  
675 680 685

Gly Ala Ser Ile Ser Gly Asn Lys Leu Phe Ile Asn Leu Gly Thr Asn  
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